Anti-DBC-1 antibody

Description	Rabbit polyclonal to DBC-1.

Model	STJ92659
Host	Rabbit
Reactivity	Human
Applications	ELISA, WB
Immunogen	Synthesized peptide derived from human DBC-1
Immunogen Region	400-480 aa, Internal
Gene ID	57805
Gene Symbol	CCAR2
Dilution range	WB 1:500-1:2000ELISA 1:20000
Specificity	DBC-1 Polyclonal Antibody detects endogenous levels of DBC-1 protein.
Tissue Specificity	Expressed in gastric carcinoma tissue and the expression gradually increases with the progression of the carcinoma (at protein level). Expressed ubiquitously in normal tissues. Expressed in 84 to 100% of neoplastic breast, lung, and colon tissues.
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Note	For Research Use Only (RUO).
Protein Name	Cell cycle and apoptosis regulator protein 2 Cell division cycle and apoptosis regulator protein 2 DBIRD complex subunit KIAA1967 Deleted in breast cancer gene 1 protein DBC-1 DBC.1 NET35 p30 DBC

Molecular Weight	102 kDa
Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:23360OMIM:607359
Alternative Names	Cell cycle and apoptosis regulator protein 2 Cell division cycle and apoptosis regulator protein 2 DBIRD complex subunit KIAA1967 Deleted in breast cancer gene 1 protein DBC-1 DBC.1 NET35 p30 DBC
Function	Core component of the DBIRD complex, a multiprotein complex that acts at the interface between core mRNP particles and RNA polymerase II (RNAPII) and integrates transcript elongation with the regulation of alternative splicing: the DBIRD complex affects local transcript elongation rates and alternative splicing of a large set of exons embedded in (A + T)-rich DNA regions. Inhibits SIRT1 deacetylase activity leading to increasing levels of p53/TP53 acetylation and p53-mediated apoptosis. Inhibits SUV39H1 methyltransferase activity. As part of a histone H3-specific methyltransferase complex may mediate ligand-dependent transcriptional activation by nuclear hormone receptors. Plays a critical role in maintaining genomic stability and cellular integrity following UV-induced genotoxic stress. Regulates the circadian expression of the core clock components NR1D1 and ARNTL/BMAL1. Enhances the transcriptional repressor activity of NR1D1 through stabilization of NR1D1 protein levels by preventing its ubiquitination and subsequent degradation . Represses the ligand-dependent transcriptional activation function of ESR2 . Acts as a regulator of PCK1 expression and gluconeogenesis by a mechanism that involves, at least in part, both NR1D1 and SIRT1 . Negatively regulates the deacetylase activity of HDAC3 and can alter its subcellular localization . Positively regulates the beta-catenin pathway (canonical Wnt signaling pathway) and is required for MCC-mediated repression of the beta-catenin pathway . Represses ligand-dependent transcriptional activation function of NR1H2 and NR1H3 and inhibits the interaction of SIRT1 with NR1H3 . Plays an important role in tumor suppression through p53/TP53 regulation; stabilizes p53/TP53 by affecting its interaction with ubiquitin ligase MDM2 . Represses the transcriptional activator activity of BRCA1 . Inhibits SIRT1 in a CHEK2 and PSEM3-dependent manner and inhibits the activity of CHEK2 in vitro .
Cellular Localization	Nucleus Cytoplasm. Recruited to chromatin, post-UV irradiation. Sequestered to the cytoplasm in the presence of MCC. Translocated to the cytoplasm during UV-induced apoptosis.
Post-translational Modifications	ATM/ATR-mediated phosphorylation at Thr-454 upon DNA damage promotes binding to SIRT1. Phosphorylation at Thr-454 promotes its sumoylation by switching the binding partner of CCAR2 from SENP1 to PIAS3. Acetylation at Lys-112 and Lys-215 by KAT8 prevents inhibitory binding to SIRT1 and increases its deacetylase activity. Genotoxic stress induces its sumoylation and sumoylation promotes the SIRT1-CCAR2

interaction which in turn inhibits SIRT1-mediated deacetylation of p53/TP53. Sumoylation leads to transcriptional activation of p53/TP53 by sequestering SIRT1 from p53/TP53. Desumoylated by SENP1.